

GENE PRECURSOR-SEQUENCE P-SEQID GENE-SEQ G-SEQID FOLDED PRECURSOR

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GAM15	CAATGAGTCCGAGATCTTCA 1 GACCTGGAGGAGGAGATATG AGGGACAATTG	TGAGTCCGAG 16 ATCTTCAGAC CTGG	GA GAG-- AGA T CAAT GTCC ATCTTC CC G GTTA CAGG TAGAGG GG G A- GAGTA A-- A
GAM16	CATATGTATGTTTCAGGGAA 2 AGCTAGGGGATGTTTTTATA GACATCACTATG	TTTTATAGAC 17 ATCACTATG	- T CAGGG GG CATA TG ATGTTT AAAGCTA G GTAT AC TACAGA TTTTGGT / C - TA--- AG
GAM17	CCACTCTATTTTGTGCATCA 3 GATGCTAAAGCATATGATAC AGAGGTACATAATGTTTGG	TATGATACAG 18 AGGTACATAA TGTT	CTC T ----- G T CCA TATT TGTC ATCA ATGC A GGT GTAA ACAATG TAGT TACG A TT- T GAGACA A A
GAM18	CCATAATGATGCAGAGAGGC 4 AATTTTAGGAACCAAGAAA GATTGTTAAGTGTTCATTT GTGG	TTAAGTGTTT 19 CAATTGTGG	- T GAGA AGGAA CCATAAT GA GCA GGCAATTTT C GGTGTTA CT TGT TTGTTAGAA C A T GAA- AGAAA
GAM19	CCATTGACAGAGAAAAAAT 5 AAAAGCATTAGTACAAATTT GTACAGAGATGG	TGACAGAAGA 20 AAAAATAAAA GCAT	--- - AGAAAAA AA CCAT TG ACAGA TAA G GGTA AC TGTTT ATT / GAG A AAAGATG- AC
GAM20	CCTCTATTGTGTGCATCAA 6 GGATAGAGATAAAAGACACC AAGGAAGCTTTAGACCAAGAT AGAGG	TATTGTGTGC 21 ATCAAGGAT AGAG	G ----- A AAA ATAGAGA T CCTCTATT TGT GC TC GG GGAGATAG ACA CG AG CC A A GATTT A GAA ACAGAAA
GAM21	GAATAGTTTTTGTCTGTACTT 7 TCTATAGTGAATAGAGTTAG GCAGGGATATTC	TAGTTTTTGC 22 TGTACTTTCT ATAG	G GTACT AG GAATA TTTTGTCT TTCTAT T CTTAT AGGGACGG GAGATA / - ATT-- AG

GAM22	<p>GCCACATACCTAGAAGAATA 8 AGACAGGGCTTGAAAGGAT TTTGCTATAAGATGGGTGGC AAGTGGT</p>	<p>TAAGATGGGT 23 GGCAAGTGGT</p>	<p>A --- GAAGAATA A - G GCCAC TACCTA AG CAGG CTT G TGGTG GTGGT TC GTTTT GGA A AACG AGAATA-- - A A</p>
GAM23	<p>GGAGACAGCGACGAAGAGCT 9 CATCAGAAACAGTCAGACTCA TCAAGCTTCTCT</p>	<p>CAGACTCATC 24 AAGCTTCTCT</p>	<p>C GAC A - C CAG GGAGA AGC GA GAG CT AT A TCTCT TCG CT CTC GA TG / - AA- A A C ACA</p>
GAM24	<p>GGTCCAAAATGCGAACCCAG 10 ATTGTAAGACTATTTTAAAA GCATTGGGACC</p>	<p>TCCAAAATGC 25 GAACCCAGAT TGTA</p>	<p>AA GAACCC T TA GGTCC AATGC AGAT G A CCAGG TTACG TTTA C / G- AAAAT- T AG</p>
GAM25	<p>GTA CTGGGTCTCTGTGTTA 11 GACCAGATCTGAGCCTGGGA GCTCTGTGGCTAACTAGGGA ACCCACTGC</p>	<p>TCTCTGGTTA 26 GACCAGATCT GAGC</p>	<p>C C A TCT CT GTA TGGGT TCTCTGGTTAG CCAGA GAGC G CGT ACCCA AGGGATCAATC GGTCT CTCG G C - - - - - AG</p>
GAM26	<p>TAATTGGAAGAAATCTGTTG 12 ACTCAGATTGGTTGCACTTT AAATTTTCCCATTA</p>	<p>TTGGTTGCAC 27 TTTAAATTTT CCCA</p>	<p>T ----- TT TAAT GGAAGA AATCTG G ATTA CCTTTT TTAGAC A C AAATTTTCACTGG TC</p>
GAM27	<p>TCTTTGGCAACGACCCCTCG 13 TCACAAATAAAGATAGGGGGG CAACTAAAGG</p>	<p>TGGCAACGAC 28 CCCTCGTCAC AATA</p>	<p>CAACGA CG ACA TCTTTGG CCCCT TC A GGAAATC GGGG AG T AACG-- AT AAA</p>
GAM28	<p>TTACCCATATAGTGCAGAAACA 14 TCCAGGGGCAAAATGGTACAT CAGGCCATATCACCTAGAAC TTTAAATGCATGGGTAA</p>	<p>TATAGTGAC 29 AACATCCAGG GGCA</p>	<p>TATA GAACA-- C GGCAA ACA TTACCC GTGCA TC AGG ATGGT T AATGGG TACGT AG TCC TACCG / ----- AAATTTCA A ACTA- GAC</p>

GAM29

TTCATTGCCCAAGTTTGTTC 15
ATAACAAAAGCCTTAGGCAT
CTCCTATGGCAGGAA

AGCCTTAGGC 30
ATCTCCTATG
GCAG

A AG-----T
TTC TTGCCA TTTGTT C
||| |||||
AAG GACGGT AAACA A
- ATCCTCTACGGATTCCGA T

GENE	TARGET	UTR	SEQUENCE	SEQID	BINDING-SITE
GAM15	PRIM2A	3'	CAGGCAGATCTCAGACTC	50	<div> <div>C</div> <div> <div>TGATC</div> <div>GAGATCT</div> <div>CCTG</div> </div> <div> <div> </div> <div> </div> <div> </div> </div> <div>CTCAG</div> <div>CTCTAGA</div> <div>GGAC</div> </div>
GAM15	RAP1B	3'	CCAGGTCTGAAGAACTGTTGCC	142	<div> <div>A</div> <div>CCG</div> <div>A</div> <div> <div>TG</div> <div>GT</div> <div>AG</div> <div>TCTTCAGACCTGG</div> </div> <div> <div> </div> <div> </div> <div> </div> <div> </div> <div> </div> </div> <div>AC</div> <div>CG</div> <div>TC</div> <div>AGAAGTCTGGACC</div> </div>
GAM15	RET	3'	CCAGGTCTAAACAGCTGACCCA	173	<div> <div>C</div> <div>TTG</div> <div>A</div> <div> <div>TG</div> <div>GTC</div> <div>AG</div> <div>AGACCTGG</div> </div> <div> <div> </div> <div> </div> <div> </div> <div> </div> <div> </div> </div> <div>AC</div> <div>CAG</div> <div>TC</div> <div>TCTGGACC</div> </div>
GAM15	RET	3'	CCAGGTCTAAACAGCTGACCCA	174	<div> <div>C</div> <div>CG</div> <div>GACAAA</div> <div> <div>TG</div> <div>GTC</div> <div>AG</div> <div>AGACCTGG</div> </div> <div> <div> </div> <div> </div> <div> </div> <div> </div> <div> </div> </div> <div>AC</div> <div>CAG</div> <div>TC</div> <div>TCTGGACC</div> </div>
GAM15	RET	3'	CCAGGTCTAAACAGCTGACCCA	179	<div> <div>C</div> <div>CG</div> <div>ATCTTC</div> <div> <div>TG</div> <div>GTC</div> <div>AG</div> <div>AGACCTGG</div> </div> <div> <div> </div> <div> </div> <div> </div> <div> </div> <div> </div> </div> <div>AC</div> <div>CAG</div> <div>TC</div> <div>TCTGGACC</div> </div>
GAM15	RET	3'	CCAGGTCTAAACAGCTGACCCA	37	<div> <div>C</div> <div>CG</div> <div>GACAAA</div> <div> <div>TG</div> <div>GTC</div> <div>AG</div> <div>AGACCTGG</div> </div> <div> <div> </div> <div> </div> <div> </div> <div> </div> <div> </div> </div> <div>AC</div> <div>CAG</div> <div>TC</div> <div>TCTGGACC</div> </div>
GAM15	AMOTL1	3'	CTGATAAAGATTTTCAGACTCA	304	<div> <div>C</div> <div>CG</div> <div>GACAAA</div> <div> <div>TGATC</div> <div>GAGATCT</div> <div>TCAG</div> </div> <div> <div> </div> <div> </div> <div> </div> </div> <div>ACTCAG</div> <div>CTTTAGA</div> <div>AGTC</div> </div>
GAM15	DGKZ	3'	CCAGACCTAGGGCTGGACTCA	70	<div> <div>A</div> <div>AAT</div> <div> <div>TGAGTCC</div> <div>AG</div> <div>TCTT</div> <div>AG</div> <div>CTGG</div> </div> <div> <div> </div> <div> </div> <div> </div> </div> <div>ACTCAGG</div> <div>TC</div> <div>GGGA</div> <div>TC</div> <div>GACC</div> </div>
GAM15	DKFZP586G1122	3'	CAGGTCTAGCCGGGCCCA	265	<div> <div>A</div> <div>AGAT</div> <div>TC</div> <div> <div>TG</div> <div>GTCCG</div> <div>CT</div> <div>AGACCTG</div> </div> <div> <div> </div> <div> </div> <div> </div> </div> <div>AC</div> <div>CGGC</div> <div>GA</div> <div>TCTGGAC</div> </div>
GAM15	FLJ22127	3'	CCAGGCCTGAATGGATGGACTC	192	<div> <div>C</div> <div>GAG</div> <div> <div>TGAGTCC</div> <div>ATCT</div> <div>TCAG</div> <div>CCTGG</div> </div> <div> <div> </div> <div> </div> <div> </div> </div> </div>

GAM15	LOC126248	3'	CAGCCCTGGCTGACTC	308	ACTCAGG TAGG AGTC GGACC G ATCT AC GAGTCC AG TCAG CT G CTCAGG TC GGTC GA C CC A - AGATCT AG TGAGTCCG TC ACCTGG ACTCAGGC AG TGGACC CCATCC - A CCG A TG GT AG TCCTCAGACCTGG AC CG TC AGAAGTCTGGACC C TTG A A CCG A TG GT AG TCCTCAGACCTGG AC CG TC AGAAGTCTGGACC C TTG A T C TTTTA AGA ATCACTATG AAAAT TCT TGGTGGTAC A - A A CTATG TTTTATAGAC TC AAAATGTCTG GG GATAC CG AC A TTTTATAGAC TCACCTATG AGAATATTG AGTGATAC AA CAC TTTTATAGACAT TATG AAGATATCTGTA GTAC AAA ATA A TTTT GAC TCACCTATG AGAA CTG AGTGATAC GTC C C A TTTTATAGA ATC CTATG
GAM15	LOC146640	5'	CCAGGTGACCTACCCGGACTCA	323	
GAM15	LOC153416	3'	CCAGGTCTGAAGAACTGTTGCC CA	263	
GAM15	LOC220790	3'	CCAGGTCTGAAGAACTGTTGCC CA	378	
GAM16	PRKG2	3'	CATGGTGGTATCTTAAAA	103	
GAM16	AFAP	3'	CATAGCAGGGCGTCTGTAAAA	183	
GAM16	C3AR1	3'	CATAGTGAAGTTTATAAGA	76	
GAM16	FLJ22029	3'	CATGAAAATGTCTATAGAA	203	
GAM16	SEMA5A	3'	CATAGTGACGTCCTGAAGA	72	
GAM16	UNC5D	3'	CATAGGATTTCTATAGAA	234	

GAM16	LOC129446	3'	CATAGAATGTCGTCTATAAA	315	<p>AAGATATCT TAG GATAC</p> <p>T CA_</p> <p>TTTATAGACAT CTATG</p> <p> </p> <p>AAATATCTGTG GATAC</p> <p>TAA</p>
GAM16	LOC153396	3'	CATAGTGGCTGCCCTATAGAA	338	<p>A A_ TCACATAG</p> <p>TTTTATAG CA_</p> <p> </p> <p>AGATATC GT GGTGATAC</p> <p>C C</p>
GAM16	LOC50999	3'	CATAATGGTGTCTTTAAAA	145	<p>T C</p> <p>TTTTA AGACATCA TATG</p> <p> </p> <p>AAAAT TCTGTGGT ATAC</p>
GAM17	KIAA0830	3'	AACATTATGCTTACTGCATC	290	<p>A TA</p> <p>GAT CAG AGG CATAATGTT</p> <p> </p> <p>CTA GTC TTC GTATTACAA</p> <p>C A</p>
GAM17	PREI3	3'	AACATTATGCTTACTGTATATATC	275	<p>ATGATA GGTACATAATGTT</p> <p> </p> <p>TACTAT TCAATGATTACAA</p> <p>ATATG</p>
GAM17	SEC15L	3'	ACATATGCCCTCTACTCATA	297	<p>TAC CATA</p> <p>TATGA AGAGGTA ATGT</p> <p> </p> <p>ATACT TCTCCGT TACA</p> <p>CA_ A_</p>
GAM17	LOC152317	3'	AACATCAATGGACTCTGTATCA	352	<p>GTA A_</p> <p>TGATACAGAG CAT ATGTT</p> <p> </p> <p>ACTATGTC TC GTA TACAA</p> <p>AG_ AC</p>
GAM18	DSCR1	3'	CATTTTGAATACTTAA	81	<p>TTT</p> <p>TTAAGTGTTC CA_ GTG</p> <p> </p> <p>AATTCATAAAGTT TAC</p>
GAM18	ELMO2	3'	CCAGGAGAAACACTTA	235	<p>AA G</p> <p>TAAGTGTTC TT TGG</p> <p> </p> <p>ATTCACAAAG AG ACC</p> <p>G</p>
GAM18	ELMO2	3'	CCAGGAGAAACACTTA	186	<p>AA G</p> <p>TAAGTGTTC TT TGG</p> <p> </p>

GAM18	PGF5	3'	CCACAGGGAGCAAAACACTTAG	227	ATTCAAAAAG AG ACC G CAA_ TTGTGG TTAAGTGTTC GATTCACAAA GACACC CGAGG
GAM18	PGF5	3'	CCACAGGGAGCAAAACACTTAG	83	CAA_ TTGTGG TTAAGTGTTC GATTCACAAA GACACC CGAGG
GAM18	NEFH	3'	CCACACGTAAACACTTGA	180	CAAT TGTTGG TTAAGTGTTC AGTTCACAAA ACACC TGC_ AA
GAM18	NFIB	3'	CCACAAAAAGAAACACTTAA	93	AA TTAAGTGTTC TTGTGG AATTCACAAAG AACACC AA
GAM18	PRKY	3'	CCATAAATGAAACACTTGA	62	A TTAAGTGTTC TTGTGG AGTTCACAAAGT AATACC A
GAM18	RNF18	5'	CCACAATTGGGTTCTTA	172	TGT TAAG TTCAATTGTGG ATTC GGGTTAACACC TT_ T
GAM18	SLC1A3	3'	CCACAATTGAAATTTTAA	77	T TTAAG GTTTC AATTGTGG AATTT TAAAGTTAACACC T
GAM18	VMD2	3'	CCATTGGAACATTTAA	78	AATT TTAAGTGTTC GTGG AATTTACAAA TACC GT_ AAT_ G
GAM18	XRCC3	5'	CCAGGGAGACACTTAA	91	T TGG TTAAGTGTTC AATTCACAGAG G ACC G
GAM18	ARHGAP5	3'	CTATATGAAACATTTAA	321	AT TTAAGTGTTC TTGTGG

GAM18	EFA6R	3'	CCATTGTGAAACACTTAA	140	AATTTCACAAAGT ATATC ATT TTTAAGTGTTC GTGG AATTACACAAAGT TACC GT- T AT- TAAGTGTT CA TGTGG AATCACAA GT ACACC T- GTGTTT CAATTGTGG TACAAG GTTAACACC TCT TTAAGTGTTT AT TGG AATTCACAAG TG GTC AA GT AA- TTAAGTGTTC TTGTGG AGTTCACAAAG AACACC GTC TGT TAAG TTCAATTGTGG ATTC GGGTTAACACC TT- TTAAGTGTTC TTG TGG AATTCACAAAG AAC ACC AA T ATT TTAAGTGTTC GTGG AATTACAAAGT CACC
GAM18	KIAA0903	3'	CCACATGTAAACACTTA	294	
GAM18	KIAA1244	3'	CCACAATTGTCTGAACAT	295	
GAM18	Rpo1-2	3'	CTGTGGTAAGAACACTTAA	214	
GAM18	LOC115574	3'	CCACAACCTGGAACACTTGA	303	
GAM18	LOC144144	5'	CCACAATTGGGTTCTTA	260	
GAM18	LOC148254	3'	CCATCAAAAGAAACACTTAA	329	
GAM18	LOC157624	5'	CCACTGAAACATTTAA	359	
GAM18	LOC220486	5'	CCACAATTGGGTTCTTA	374	
GAM19	AGL	3'	ATGCTTTCATTTTTTCACCTG	31	TGT TAAG TTCAATTGTGG ATTC GGGTTAACACC TT- AA- CAG GAAAAAAT AAAGCAT

Gene	Accession	Position	Sequence	Length
GAM19	AGL	3'	ATGCTTTTCATTTTTTCACTG	43
			<p>GTC CTTTTTTA TTTTCGTA</p> <p>A⁻ C</p> <p>AA A</p> <p>CAG GAAAAAAT AAAGCAT</p> <p> </p> <p>GTC CTTTTTTA TTTTCGTA</p>	
GAM19	AGL	3'	ATGCTTTTCATTTTTTCACTG	44
			<p>GTC CTTTTTTA TTTTCGTA</p> <p>A⁻ C</p> <p>AA A</p> <p>CAG GAAAAAAT AAAGCAT</p> <p> </p> <p>GTC CTTTTTTA TTTTCGTA</p>	
GAM19	AGL	3'	ATGCTTTTCATTTTTTCACTG	45
			<p>GTC CTTTTTTA TTTTCGTA</p> <p>A⁻ C</p> <p>AA A</p> <p>CAG GAAAAAAT AAAGCAT</p> <p> </p> <p>GTC CTTTTTTA TTTTCGTA</p>	
GAM19	AGL	3'	ATGCTTTTCATTTTTTCACTG	46
			<p>GTC CTTTTTTA TTTTCGTA</p> <p>A⁻ C</p> <p>AA A</p> <p>CAG GAAAAAAT AAAGCAT</p> <p> </p> <p>GTC CTTTTTTA TTTTCGTA</p>	
GAM19	AGL	3'	ATGCTTTTCATTTTTTCACTG	47
			<p>GTC CTTTTTTA TTTTCGTA</p> <p>A⁻ C</p> <p>AA A</p> <p>CAG GAAAAAAT AAAGCAT</p> <p> </p> <p>GTC CTTTTTTA TTTTCGTA</p>	
GAM19	ALB	5'	GCTTTTCTCTTCTGTCA	40
			<p>TGACAGAGA</p> <p> </p> <p>ACTGTCCTCT</p> <p>AAAAAT</p> <p>AAAAAGC</p> <p>TTTTCG</p>	
GAM19	CKN1	3'	TTTTATTCTTTCTCTTCA	32
			<p>TGA AGAAGAAA AATAAAA</p> <p> </p> <p>ACT TCCTCTTT TTAATTT</p> <p>C</p>	
GAM19	HHIP	3'	TTTTATTTTTTATCCTGTCA	189
			<p>- AAG</p> <p>TGACAG AAAAAATATA</p> <p> </p> <p>ACTGTC TTTTTTATTT</p> <p>CTA</p>	
GAM19	IFNA1	3'	GCTTTTCATGAATTCGTCA	194
			<p>TGACAGAA AT AAAGC</p> <p> </p> <p>ACTGTC TT TTTTCG</p> <p>GAAGAA A</p>	
GAM19	KCNJ6	5'	TTTTTTTTTTTCTTCTGTCCA	60
			<p>A</p> <p>TG CAGAAGAAAA AAAA</p> <p> </p> <p>TA TTTTCG</p> <p>AAG C</p> <p>T</p>	

GAM19	OTP	3'	GCTTTTATTTTATTTTATC	212	AC GTCTTCTTTTTT TTTT C C GA GA AGAA AAAAAATAAAAGC CT TTTT TTTTATTTTCG A A_ TAA TGACAGAAAGAAAAA AAGCAT ATTGCTTCTTTTTT TTCGTA C_
GAM19	RHEB2	3'	ATGCTTCTTTTTTCTTCTGTGA	94	AGAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA CCC_ ATAAAA C AGAAGAAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA
GAM19	ANKRD6	3'	ATGCTTTTATTCCTTTTGTTA	137	AGAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA CCC_ ATAAAA C AGAAGAAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA
GAM19	EVI5	3'	TGCAGGTTTTTCTTCTTCA	95	AGAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA CCC_ ATAAAA C AGAAGAAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA
GAM19	FLJ00026	3'	ATGCTTTGCTTTTTTCTTTATG	270	AGAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA CCC_ ATAAAA C AGAAGAAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA
GAM19	GP5	3'	ATGCTCATATCATTTTCTTCT	84	AGAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA CCC_ ATAAAA C AGAAGAAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA
GAM19	KHDRBS3	3'	ATGCTAGTTTTTTTTTCTTCTT	107	AGAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA CCC_ ATAAAA C AGAAGAAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA
GAM19	KIAA0254	3'	TGCTGTGTTCTTTCTGTCA	132	AGAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA CCC_ ATAAAA C AGAAGAAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA
GAM19	KIAA1165	3'	ATGCTTTTATAACCTCTTCTGT	281	AGAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA CCC_ ATAAAA C AGAAGAAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA
GAM19	KIAA1240	3'	GTGGCCATTTTCTTCTGTCA	277	AGAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA CCC_ ATAAAA C AGAAGAAAAA TGACAGA AATAAAAGCAT ATTGTTT TTAATTTTCGTA

GAM19	NYD-SP15	3'	ATGCCATTTTTTTTCTTCTGT	209	ACTGTCCTCTTTTTTA TG CCGG TAAAA ACAGAAGAAAAA GCAT TGTCTTCTTTTT CGTA TTAC_
GAM19	PEL11	5'	GCTTTACTCTTTCTTCTGTC	175	AAATA_ AAAGC GACAGAAGAAA CTGCTTCTTT TTTCG CTCA_
GAM19	PRO0159	5'	TTATTTTTCCTTGCA	125	AA TGACAG GAAAAAATAA ACTGTT CTTTTTATT C_
GAM19	RACGAP1	3'	ATGTGAGCTTTTCTTCTGTTA	121	ATAAAA GCAT TGACAGAAGAAAA ATTGCTTCTTTTT TGTA CGAG_
GAM19	SDFR1	3'	TTATCTTTTCTTCTGTTA	118	A TGACAGAAGAAAA ATAA ATTGCTTCTTT TATT C
GAM19	SDFR1	3'	TTATCTTTTCTTCTGTTA	151	A TGACAGAAGAAAA ATAA ATTGCTTCTTT TATT C
GAM19	SS18L1	3'	TTATCTATCTTCTGTC	272	AAA TGACAGAAGA AATAA ACTGCTTCT TTATT ATC
GAM19	SV2B	3'	ATGTTTACTCTCTTCTGTC	136	ATC AAAAAATAA AAGCAT TGACAGAAG ACTGCTTCT TTTGTA CTCTCA_
GAM19	LOC130589	3'	TGCTTTTATTTCTCTCTCTTC	244	CA A AA TGA GA GA AATAAAGCA ACT CT CT TTTATTTTCGT TC C CC
GAM19	LOC200107	3'	ATGCTTTTACTTTTCTTTT	364	A AGAAGAAAA TAAAGCAT

GAM19	LOC203340	3'	TGCTTTTATTTTCCTTC	368	TTTTCTTTTT ATTTTCGTA C AA GAAG AAAATAAAAGCA CTTC TTTTATTTTCGT C- ATAAAA TGACAGAGAAAAA GCA ACTGTCCTTTTTTTT CGT C C AAATAAA TGA AGAAGAAA AGCAT ACT TCTTCCTT TCGTA A A A AGA GA AAAATAAAAGC TCT CT TTTTATTTTCG C C TGACAGAGAA AAAATAAAAG -ACTGTCCTTTT TTTATTTT C AAAA GAAG AATAAAAGCAT CTTC TTTTATTTTCGTA CATG A AAA ACAGAGAAAA AT GCA TGTCCTCTTT TA CGT C G AAG TT TGTGCATCA GATAG AA ACACGTAGT CTATC G G AAG TT TGTGCATCA GATAG AA ACACGTAGT CTATC G TATTGTGTGCAT AGGA AGAG
GAM19	LOC221271	3'	TGCCCTTTTTTTTCGTCA	380	
GAM19	LOC254778	3'	ATGCTTTTCTTCTATCA	400	
GAM19	LOC51312	5'	GCCTTTTATTTTCTCCTCT	164	
GAM19	LOC91286	5'	TTTTTATTTCTTTTCTGTCA	273	
GAM19	LOC92223	3'	ATGCTTTTATGTACCTTC	286	
GAM19	LOC92482	5'	TGCATCTTTTCTTCTGT	288	
GAM20	ATRN	3'	CTATCTGATGCACAGAA	248	
GAM20	ATRN	3'	CTATCTGATGCACAGAA	248	
GAM20	DKFZP564O0463	3'	CTTTTCTTTAATGCATACATA	127	CAA T TATTGTGTGCAT AGGA AGAG

Accession	Gene	Position	Sequence	Length	Conserved Domains
GAM20	DKFZP564O0463	3'	CTTTTCTTAATGCATACAATA	127	ATAACATACGTA TTCT TTTC A__CAA T TATTGTGTGCAT AGGA AGAG T ATAACATACGTA TTCT TTTC
GAM20	FLJ13102	3'	CTCTACCCCTCTCCCACCACACA	202	CATCAA_ A TATTGTGTG AGG TAGAG ATGACACAC TCC ATCTC CACCTC C CATCAA_ A TATTGTGTG AGG TAGAG ATGACACAC TCC ATCTC CACCTC C
GAM20	FLJ13102	3'	CTCTACCCCTCTCCCACCACACA	202	CATCAA_ A TATTGTGTG AGG TAGAG ATGACACAC TCC ATCTC CACCTC C
GAM20	HSPC014	3'	CTGTAATTTGATGTACACAA	144	CATCAA_ A TATTGTGTG AGG TAGAG ATGACACAC TCC ATCTC CACCTC C
GAM20	HSPC014	3'	CTGTAATTTGATGTACACAA	144	CATCAA_ A TATTGTGTG AGG TAGAG ATGACACAC TCC ATCTC CACCTC C
GAM20	KIAA0040	3'	TCTATCCCCTTTGTGCACATA	129	TCAA TATTGTGTGCATCAA ATAG AACACATGTAGTT TGTC AA TCAA TATTGTGTGCATCAA ATAG AACACATGTAGTT TGTC AA
GAM20	KIAA0040	3'	TCTATCCCCTTTGTGCACATA	129	TCAA TATTGTGTGCATCAA ATAG AACACATGTAGTT TGTC AA
GAM20	KIAA0040	3'	TCTATCCCCTTTGTGCACATA	129	TCAA TATTGTGTGCATCAA ATAG AACACATGTAGTT TGTC AA
GAM20	KIAA0470	3'	CCACTTGTGATGCACAAATA	134	G TATT TGTGCATCAA GG ATAA ACACGTAGTT CC CA G TATT TGTGCATCAA GG ATAA ACACGTAGTT CC CA
GAM20	KIAA0470	3'	CCACTTGTGATGCACAAATA	134	G TATT TGTGCATCAA GG ATAA ACACGTAGTT CC CA
GAM20	KIAA1908	5'	CTCTCGGGCGATGCACACAA	302	AAAGGAT TTGTGTGCATC AGAG

GAM20	KIAA1908	5'	CTCTCGGGCGGATGCACACAA	302	AACACACGTAG TCTC CGGGC AAAGGAT TTGTGTGCATC AGAG AACACACGTAG TCTC CGGGC TGCATCA TATTGTG AAGGATAGAG ATAACAC TTCCTATCTC TATATG TGCATCA TATTGTG AAGGATAGAG ATAACAC TTCCTATCTC TATATG G G TTGT TGCATCAAAG ATAG AACA ACGTAGTTTT TGTC A G G TTGT TGCATCAAAG ATAG AACA ACGTAGTTTT TGTC A GGA TATTGTGTGCATCAAA TAGAG ATAACATACGTAGTTT GTTTC G GGA TATTGTGTGCATCAAA TAGAG ATAACATACGTAGTTT GTTTC G AAAG GATAG TGTTGTGCATC ACACACGTAG CTATC GTGTA AAAG GATAG TGTTGTGCATC ACACACGTAG CTATC GTGTA T G CAAA TATTG GT CAT GGATAGAG
GAM20	MGC22014	3'	CTCTATCCCTTGTTATATCAACAAT	269	
GAM20	MGC22014	3'	CTCTATCCCTTGTTATATCAACAAT	269	
GAM20	TNRC9	3'	CTGTATTTTGATGCAACAA	293	
GAM20	TNRC9	3'	CTGTATTTTGATGCAACAA	293	
GAM20	LOC116123	3'	CTTTGGTTTGATGCATACAATA	243	
GAM20	LOC116123	3'	CTTTGGTTTGATGCATACAATA	243	
GAM20	LOC149721	3'	CTATCATGTGGATGCACACA	334	
GAM20	LOC149721	3'	CTATCATGTGGATGCACACA	334	
GAM20	LOC153338	5'	CTCTATCCCTCTGTGGCCAATA	354	

GAM20	LOC153338	5'	CTCTATCCCTCTGTGGCCAATA	354	ATAAC CG GTG CCTATCTC TCTC T G CAAA TATTG GT CAT GGATAGAG ATAAC CG GTG CCTATCTC TCTC
GAM20	LOC220766	3'	CCACTTGATGCACAAATA	375	G - - A - TATT TGTGCATCAA GG ATAA ACACGTAGTT CC CA
GAM20	LOC220766	3'	CCACTTGATGCACAAATA	375	G - - A - TATT TGTGCATCAA GG ATAA ACACGTAGTT CC CA
GAM20	LOC253351	5'	CTGGCACCTGATGCACAAA	402	- AAGGA TTGTGTGCATCA TAG AACACACGTAGT GTC CCACG
GAM20	LOC253351	5'	CTGGCACCTGATGCACAAA	402	AAGGA TTGTGTGCATCA TAG AACACACGTAGT GTC CCACG
GAM20	LOC257484	3'	CTCTATCCCTTGTTATATACAAT	366	TGTCATCA TATTGTG AAGGATAGAG ATAACAC TTCCTATCTC TATATG
GAM20	LOC257484	3'	CTCTATCCCTTGTTATATACAAT	366	TGTCATCA TATTGTG AAGGATAGAG ATAACAC TTCCTATCTC TATATG
GAM21	KIAA1843	3'	ATAGAAAAGTAGCCAAAAA	267	CTG TTTTTG TACTTTCTAT AAAAAC ATGAAAAGATA CG -
GAM21	SDFR1	3'	AAAGTACAGCAAAACCTA	117	T TAG TTTTGTCTGTACTTT ATC AAAACGACATGAAA C
GAM21	SDFR1	3'	AAAGTACAGCAAAACCTA	150	T TAG TTTTGTCTGTACTTT

GAM21	LOC132617	3'	CTACAGACCATAGCAAAAAC	314	ATC AAAACGACATGAAA C ACCTT A GTTTTTGCTGT TCT TAG CAAAAACGATA AGA ATC CC C TGTACT GTTTTTGC TTCTATAG CAAAAACG AAGATATC TAAC G CT A TAGTTTTTGCT TA TTCT TAG ATCAAAAACGA GT AAGA ATC G AC C G CT A TAGTTTTTGCT TA TTCT TAG ATCAAAAACGA GT AAGA ATC G AC C G CT A TAGTTTTTGCT TA TTCT TAG ATCAAAAACGA GT AAGA ATC G AC C G CT A AGATGGGTG AGTGGT TCTACCTAC TCACCA A T CAA AAGATGGG GG GTGGT TTCTACTT CC CACCA TC CA T AGATGGGTGG AG GGT TCTACCCACC TC CCA CCG
GAM21	LOC145622	3'	CTATAGAACAAATGCAAAAAC	322	
GAM21	LOC222681	3'	CTACAGAACATGGAGCAAAAAC TA	386	
GAM21	LOC257507	3'	CTACAGAACATGGAGCAAAAAC TA	405	
GAM21	LOC257625	3'	CTACAGAACATGGAGCAAAAAC TA	406	
GAM22	BTEB1	3'	ACCACTACATCCATCT	53	
GAM22	CEP2	3'	ACCACCTCCTTCATCTT	112	
GAM22	ECM1	3'	ACCCTGCCCCACCCATCT	82	
GAM22	ENG	3'	ACCACITGGCCACGCTGTT	34	
GAM22	ESRRG	3'	ACCACITTTTCAGCCATTT	276	G C AGATGG TGG AAGTGGT

GAM22	HDAC4	3'	ACCACTCGACTCATCTTG	98	TTTACC ACT TTCACCA G T GGCA TAAGATGGGT AGTGGT GTTCTACTCA TCACCA
GAM22	IL6	3'	ACCACTTGAAACATTTTA	41	GC GGTGG TAAGATG CAAGTGGT ATTTTAC GTTCACCA
GAM22	LPAT	3'	ACCACTTAAAAATATCTTA	259	AAA GTGGC TAAGATGG AAGTGGT ATTCTATT TTCACCA
GAM22	MYLK2	3'	ACCACTCGGGGCCCCCATCTTG	226	AAAA T A TAAGATGG GGC AGTGGT GTTCTACCC CCG TCACCA
GAM22	PRKACB	3'	ACCACTTCTTTTCATCT	61	GGGC T C AGATGGG GG AAGTGGT TCTACTT TC TTCACCA
GAM22	PRLR	3'	ACCACTTGCCCTCTTTCT	51	T T AGA GGG GGCAAGTGGT TCT TCT CCGTTCACCA
GAM22	SLC6A6	3'	ACCACTTGAATTGATCTT	65	T G GG AAGAT GGT CAAGTGGT TTCTA TTA GTTCACCA
GAM22	WASF3	3'	ACCACTTGGTCAGAAATTTTA	109	G A GGG TAAGAT TGGC AAGTGGT ATTTTA ACTG TTCACCA
GAM22	XK	3'	ACCACTTGCACTATTCTTA	181	AG G TG G TAAGA GGTG CAAGTGGT ATTCT TCAC GTTCACCA
GAM22	ZYX	3'	ACCACCTGCCCCCACT	69	TA A T A AG TGGG GGCA GTGGT

GAM22	ARHF	3'	ACCTGGACCA	167	TC ACCC CCGT CACCA C - CA_ T AGATGGGTGG AG GGT TCTACCCACC TC CCA AGG - CAA - TAAGATGGGTGG GTG ATTTTACCCACC CGC A - CAA TAAGATGGGTGG GTG ATTTTACCCACC CGC A - CAA TAAGATGGGTGG GTG ATTTTACCCACC CGC A - TG CAA TAAGATGGG G GTGGT ATTCTATCC C CACCA CT - TG CAA TAAGATGGG G GTGGT ATTCTATCC C CACCA CT - AA AGATGGGT GGC GTGGT TCTACCCG CCG CGCCA AC AAG AGATGG GTGC TGGT TCTACC CGCCG ACCA TA GG - T GA GGGT GGCAAGTGGT CT TCCG CCGTTCACCA C TAA TG GGT GGCAAGTGGT
GAM22	DDR1	5'	CGCACCA	57	
GAM22	DDR1	5'	CGCACCA	122	
GAM22	DDR1	5'	CGCACCA	123	
GAM22	DKFZP547E1010	5'	ACCACCTCCCTATCTTA	141	
GAM22	DKFZP547E1010	5'	ACCACCTCCCTATCTTA	280	
GAM22	FLJ11715	3'	ACCGGCGCCAGCCCATCT	197	
GAM22	FLJ12587	3'	ACCAGGGCGCATCCATCT	190	
GAM22	FLJ12650	3'	ACCACCTGGCCAATGCCCTCTC	196	
GAM22	FLJ13265	3'	ACCACCTGGCCCTGCCCTCA	201	

GAM22	FLJ20546	3'	ACCTCTGCCACCCATCT	155	AC CCG CCGTTCACCA T TC A T AGATGGGTGGCA G GGT TCTACCCACCGT C CCA T
GAM22	FLJ32865	3'	ACCACCAGCCCAGCTTA	251	A GCAA TAAAG TGGGTG GTGGT ATTC ACCCGC CACCA G AC
GAM22	GPR88	3'	ACCACTTGTTGTACATCT	185	G TG AGATG G GCAAGTGGT TCTAC T TGTTACCA A GT
GAM22	HSPC216	3'	ACCTGACCACCCATTT	149	AGATGGGTGG CA GGT TTTACCCACC GT CCA A
GAM22	JK	3'	ACCACATTCCCCATTTTA	148	T CAA TAAAGTGGG GG GTGGT ATTTTACCC CT CACCA TA
GAM22	KIAA0153	3'	ACCACCAGCAAGCCCGCCTTA	139	A G AA TAAG TGGGT GC GTGGT ATTC GCCCG CG CACCA C AA ACC
GAM22	KIAA0215	3'	ACCAGGAGACCACCATCTTA	130	G CAAG TAAGATGG TGG TGGT ATTCTACC ACC ACCA AGAGG
GAM22	KIAA0461	3'	ACCACTTGTTGAAATCCA	291	TGGGT GGCAAGTGGT ACCTA TTGTTACCA AAG
GAM22	MEGF10	3'	ACCACAGACTCATCTTA	216	GGCAA TAAGATGGGT GTGGT ATTCTACTCA CACCA GA
GAM22	MGC2452	5'	ACCACTAAATTGCCACTCA	218	TGGGTGGCA AGTGGT

GAM22	MGC4796	3'	ACCTTCACCTCATCTTTA	266	ACTCACCGT TCACCA TAA TAAAGATG_GGTGG GGT ATTCTAC CCACT CCA T T T G AGATGGGTG CAA GTGGT TTTACCCAT GTT CACCA
GAM22	MRPL10	3'	ACCACATTGTACCCATTTT	256	GG_G TAAGATG TG CAAGTGGT GTTCTAC AT GTTCACCA GA A AAGATGGGTGGCA GTGGT TTCTACCTATCGT CACCA
GAM22	MRPL42	5'	ACCACTTGATAAGCATCTTG	299	GG_G TAAGATG TG CAAGTGGT GTTCTAC AT GTTCACCA GA A AAGATGGGTGGCA GTGGT TTCTACCTATCGT CACCA
GAM22	POLYDOM	3'	ACCACTTGCTATCCATCTTT	195	GG AGAT GTGGCAAGTGGT TCTG TATCGTTCACCA G_
GAM22	PRO0246	5'	ACCACTTGCTATGGTCT	126	A G AG TGGGTGGCAAGT GT TC ACCCACCGTTCA TA C G ATG GC TAAG GGTG AAGTGGT ATTC CTAT TTCACCA AA_ A_CA
GAM22	SMCR7	3'	ATGACTTGCCACCCACCT	247	AAGATGG GTGG AGTGGT TTCTACC CACT TCACCA GG AC CA T TAAGATGGGTGG AG GGT ATTCTACCCACT TC GCA CC T AA AGATGGGTG GC GTGGT
GAM22	TPD52	3'	ACCACCTTATATCAACTTA	88	AA_ A_CA AAGATGG GTGG AGTGGT TTCTACC CACT TCACCA GG AC CA T TAAGATGGGTGG AG GGT ATTCTACCCACT TC GCA CC T AA AGATGGGTG GC GTGGT
GAM22	ZNF384	3'	ACCACTCATCAGGCCATCTTT	239	AA_ A_CA AAGATGG GTGG AGTGGT TTCTACC CACT TCACCA GG AC CA T TAAGATGGGTGG AG GGT ATTCTACCCACT TC GCA CC T AA AGATGGGTG GC GTGGT
GAM22	LOC124216	3'	ACCTCTCCTCACCCTCTTA	307	AA_ A_CA AAGATGG GTGG AGTGGT TTCTACC CACT TCACCA GG AC CA T TAAGATGGGTGG AG GGT ATTCTACCCACT TC GCA CC T AA AGATGGGTG GC GTGGT
GAM22	LOC144509	5'	ACCACCAAGCTGACCCCATCT	320	AA_ A_CA AAGATGG GTGG AGTGGT TTCTACC CACT TCACCA GG AC CA T TAAGATGGGTGG AG GGT ATTCTACCCACT TC GCA CC T AA AGATGGGTG GC GTGGT

GAM22	LOC146822	3'	ACCACCTGCCCTACCATTT	324	<p>TCTACCCAC CG CACCA</p> <p>GT AC</p> <p>GT_ A</p> <p>AGATGG GGCA GTGGT</p> <p> </p> <p>TTTACC CCGT CACCA</p> <p>ATC C</p> <p>G C</p> <p>AGATGG TGG AAGTGGT</p> <p> </p> <p>TCTACC GTC TTCACCA</p> <p>G</p> <p>A _ AA</p> <p>A GATGGTGGC GT GGT</p> <p> </p> <p>A TTACCCACCG CG CCA</p> <p>C GC T</p> <p>TAAGATGGG TGG GGT</p> <p> </p> <p>ATTCTACCC ACC CCA</p> <p>G CC</p> <p>G CAA</p> <p>TAAGATGG TGG GTGGT</p> <p> </p> <p>ATTTTACT ACC CACCA</p> <p>G</p> <p>TAAGATG GGTG AAGTGGT</p> <p> </p> <p>ATTCTAC CCGT TTCACCA</p> <p>T AATA</p> <p>G A</p> <p>AGATGG TGGCA GTGGT</p> <p> </p> <p>TCTACC GTCGT CACCA</p> <p>G</p> <p>TGGG TGGCAAGTGGT</p> <p> </p> <p>ATCC GCCGTTACCA</p> <p>TCGA</p> <p>G AAG</p> <p>TAAGATGGGT GC TGGT</p> <p> </p> <p>ATTCTATCCA TG ACCA</p> <p>A</p> <p>G CA</p> <p>AGATGG TGG AGTGGT</p> <p> </p>
GAM22	LOC148371	5'	ACCATTCTGGCCATCT	330	
GAM22	LOC149373	3'	ACCTGCCGGCCACCCATTCA	333	
GAM22	LOC151146	5'	ACCCCCAGCCCATCTTA	336	
GAM22	LOC157562	5'	ACCACCCAGTCATTTTA	357	
GAM22	LOC160897	3'	ACCATTATAATGCCCTCATCTT	341	<p>A</p>
GAM22	LOC161589	5'	ACCACCTGCTGGCCATCT	343	
GAM22	LOC163682	5'	ACCATTGCGGAGCTCCTA	361	
GAM22	LOC199692	3'	ACCAGTAACCTATCTTA	257	
GAM22	LOC202108	5'	ACCACTACTGGCCATCT	367	

GAM22	LOC221468	3'	ACCACCCAGTTTCTTCATCTT	258	<p>TCTACC GTC TCACCA</p> <p>G A_ TG AA_</p> <p>AAGATGG GC GTGGT</p> <p> </p> <p>TTCTACTT TG CACCA</p> <p>CT ACC</p>
GAM22	LOC221838	5'	ACCACTACTGGCCATCT	385	<p>G CA</p> <p>AGATGG TGG AGTGGT</p> <p> </p> <p>TCTACC GTC TCACCA</p>
GAM22	LOC221839	5'	ACCACTACTGGCCATCT	384	<p>G A_</p> <p>G CA</p> <p>AGATGG TGG AGTGGT</p> <p> </p> <p>TCTACC GTC TCACCA</p>
GAM22	LOC90313	5'	ACCACCCCTGTGCCCATC	268	<p>G A_</p> <p>G A_</p> <p>GATGGTG CA GTGGT</p> <p> </p> <p>CTACCCGT GT CACCA</p> <p>CCC</p>
GAM22	LOC92399	3'	ACCACCTGTCTCTCATCTTA	242	<p>-TG A</p> <p>TAAGATGG GCA GTGGT</p> <p> </p> <p>ATTCTACTC CGT CACCA</p> <p>CT C</p>
GAM23	ADAM8	3'	AGAGAAGCCATGCGTTCC	52	<p>A T CAA</p> <p>C GAC CAT GCTTCTCT</p> <p> </p> <p>C TTG GTA CGAAGAGA</p> <p>C C C_ AA_ T</p>
GAM23	BN51T	3'	AGAGAGCAAGGATTGAGTCTG	363	<p>CAGACTCA TC GCT CTCT</p> <p> </p> <p>GTCTGAGT AG CGA GAGA</p> <p>T GAA</p>
GAM23	CD3Z	3'	AGACTGACCTTGATGAGCTG	48	<p>A C C_</p> <p>CAG CTCATCAAG TT TCT</p> <p> </p> <p>GTC GAGTAGTTC AG AGA</p> <p>-C T</p>
GAM23	DAAM2	3'	AGGTGCTTGATGAATCTG	381	<p>CAGA TCATCAAGC TCT</p> <p> </p> <p>GTCT AGTAGTTCG GGA</p> <p>A T</p>
GAM23	DLG4	3'	AGGAGGGATGGGTCT	54	<p>AAG</p> <p>AGACTCATC CTTCTCT</p> <p> </p>

GAM23	DMD	5'	AGAAAAGCTTGAGCAAGTC	73	<p>TCTGGGTAG GGAGGGA</p> <p>CA_ C</p> <p>GACT TCAAGCTT TCT</p> <p> </p> <p>CTGA AGTTCGAA AGA</p> <p>ACG A</p>
GAM23	DMD	5'	AGAAAAGCTTGAGCAAGTC	74	<p>CA_ C</p> <p>GACT TCAAGCTT TCT</p> <p> </p> <p>CTGA AGTTCGAA AGA</p> <p>ACG A</p>
GAM23	DMD	5'	AGAAAAGCTTGAGCAAGTC	75	<p>CA_ C</p> <p>GACT TCAAGCTT TCT</p> <p> </p> <p>CTGA AGTTCGAA AGA</p> <p>ACG A</p>
GAM23	E2F1	3'	AGGCCTCTTTGGTGAGCCCTG	348	<p>A</p> <p>CAG CTCATCAA GCTT</p> <p> </p> <p>GTC GAGTGGTT CGGA</p> <p>C TCTC</p>
GAM23	EBP	3'	AGAGAAAGCCAGGAGGTCT	108	<p>CA AA</p> <p>AGACT TC GCTTCTCT</p> <p> </p> <p>TCTGG AG CGAAGAGA</p> <p>GAC</p>
GAM23	FANCG	5'	AGAGAAAGCAGGGAGCTC	85	<p>A AA</p> <p>GA CTC TC GCTTCTCT</p> <p> </p> <p>CT GAG GG CGAAGAGA</p> <p>C GA</p>
GAM23	FE65L2	5'	AGGCGCCTGATGAGTTCA	99	<p>A T</p> <p>C GACTCATCA GC TCT</p> <p> </p> <p>A TTGAGTAGT CG GGA</p> <p>C C C</p>
GAM23	FE65L2	5'	AGGCGCCTGATGAGTTCA	236	<p>A T</p> <p>C GACTCATCA GC TCT</p> <p> </p> <p>A TTGAGTAGT CG GGA</p> <p>C C C</p>
GAM23	FE65L2	5'	AGGCGCCTGATGAGTTCA	237	<p>A T</p> <p>C GACTCATCA GC TCT</p> <p> </p> <p>A TTGAGTAGT CG GGA</p> <p>C C C</p>
GAM23	FE65L2	5'	AGGCGCCTGATGAGTTCA	238	<p>A T</p> <p>C GACTCATCA GC TCT</p> <p> </p> <p>A TTGAGTAGT CG GGA</p> <p>C C C</p>

Gene	Accession	Position	Sequence	Length	Annotations
GAM23	FGFR4	3'	AGAGAAGCTGGAAGCCTG	193	A TTGAGTAGT CG GGA C A CA A CAG CT TC AGCTTCTCT GTC GA AG TCGAAGAGA C G A CA A CAG CT TC AGCTTCTCT GTC GA AG TCGAAGAGA C G CT A GA CATCA GCTTCTCT CT GTAGT CGAAGAGA CC
GAM23	FGFR4	3'	AGAGAAGCTGGAAGCCTG	58	
GAM23	FHL1	3'	ACAGAAGCTGATGCCTC	55	CT G G A GTC GA AG TCGAAGAGA C G CT A GA CATCA GCTTCTCT CT GTAGT CGAAGAGA CC
GAM23	GCNT2	5'	AGAGAAACGAGTGAGTTTG	56	CAAGC CAGACTCAT TTCTCT GTTTGAGTG AAGAGA AGCA CTC A CAGA ATCA GCTTCTCT GTCT TGGT CGAAGAGA TAA
GAM23	GNRHR	5'	AGAGAAGCTGGTAATTCTG	38	
GAM23	HIS1	5'	AGGGGAGATGAGTTTG	105	AAG CAGACTCATC CTTCT GTTTGAGTAG GGGGA A CAA C CAGACTCAT GCTT TCT GTTTGAGTA TGGA AGA A CAA C CAGACTCAT GCTT TCT GTTTGAGTA CGAA AGA C G C CA CA ACT AT AGCTTCTCT GT TGA TA TCGAAGAGA G A C ACT T A CAG CA CA GCTTCTCT
GAM23	HNRPDL	3'	AGAAAAGGTATGAGTTTG	92	
GAM23	INHBA	3'	AGAAAAGCCATGAGTTTG	59	
GAM23	KIF3B	3'	ACAGAAGCTCATAAGTGTG	87	
GAM23	MSN	3'	AGAGAAGCCTGTGCCCTG	262	

GAM23	MTR	3'	AGAGAAGTGTGACCCCTG	36	GTC GT GT CGAAGAGA CC_ C AC _CAA CAG TCAAT GCTTCTCT GTC AGTG TGAAGAGA
GAM23	PCDHB9	3'	AGAGAAGTTAGATCCTG	169	CC_ A ACTC _ CAG ATC AGCTTCTCT GTC TAG TTGAAGAGA
GAM23	SMARCA3	3'	AGAGAAGCTTCATGTTTG	246	C_ A TCATC CAGAC AAGCTTCTCT GTTTG TTCGAAGAGA
GAM23	SMARCA3	3'	AGAGAAGCTTCATGTTTG	66	TAC TCATC CAGAC AAGCTTCTCT GTTTG TTCGAAGAGA
GAM23	SMG1	3'	AGACAGTAGATGAGTCTG	138	TAC_ AA CAGACTCATC GCT_TCT GTCTGAGTAG TGA AGA
GAM23	SNCAIP	5'	AGAAAGGGGTGAGTCTG	399	A_ C AAG C CAGACTCATC CTT TCT GTCTGAGTGG GAA AGA
GAM23	SYNGR1	3'	AGGGGAGCGATGAGCTG	86	GG_ - A AA_- CAG CTCATC GCTTCTCT GTC GAGTAG CGAGGGGA
GAM23	UCP2	5'	AGAGAAGCTTGATCTTGGAG	68	_- CTC_ ATCAAGCTTCTCT GAG TAGTTCGAAGAGA
GAM23	BMF	3'	AGAGGCTGATGTGTCTG	229	GTTC T A CAGAC CATCA GCITCT GTCTG GTAGT CGGAGA
GAM23	BNIP2	3'	AGAGAATGTGATGAGTT	278	T AG_ GACTCATCA TTCTCT

GAM23	DDX33	3'	AGAGAAGCCTTGAATC	171	TTGAGTAGT AAGAGA GT - C AT GA TC CAAG CTCTCTCT CT AG GTTC GAAGAGA A - C GACTCATC AAG TTCT TTGAGTAG TTC AAGA GT A CAAG AGACTCAT CTCTCTCT TCTGGGTA GAAGAGA AA A CA AA CAG CT TC GCTTCTCT GTC GG AG CGAAGAGA C CA A A T T A AG C CA CA GCTTCTCT TC G GT GT CGAAGAGA - - - C A - G T CAG CTCATCAA C TCT GTC GAGTAGTT G AGA G T A - G T CAG CTCATCAA C TCT GTC GAGTAGTT G AGA G T C - TCAA CAGA TCA GCTTCTCT GTCT GGT CGAAGAGA AC TGA CA A GACT TC AGCTTCTCT CTGA AG TCGAAGAGA A AC CA CAG TCAT AGCTTCTCT
GAM23	EML4	3'	AGAAACTTTGGATGAGTT	168	
GAM23	EPB41L4	3'	AGAGAAGAAATGGGTCT	187	
GAM23	FLJ11588	5'	AGAGAAGCAGAACGGCCTG	199	
GAM23	FLJ20150	3'	AGAGAAGCCTGTGGCT	153	
GAM23	FLJ20507	3'	AGATGTTGATGAGGCTG	154	
GAM23	FLJ20507	3'	AGATGTTGATGAGGCTG	261	
GAM23	FLJ20972	3'	AGAGAAGCAGTTGGCATCTG	205	
GAM23	FLJ22233	3'	AGAGAAGCTAGAAGTC	204	
GAM23	FLJ23191	3'	AGAGAAGTTGTGACCTG	198	

GAM23	FLJ23468	5'	AGAGAAACCAAGTCAGTCTG	200	GTC AGTG TTGAAGAGA C_ TCAA TCTCT CAGACTCA GCT TCTCT GTCTGAGT CGA AGAGA CCA
GAM23	GIT2	3'	AGAGAAGCATCAGTCT	133	C CAA CCA AGACT AT GCTTCTCT TCTGA TA CGAAGAGA
GAM23	GIT2	3'	AGAGAAGCATCAGTCT	231	C CAA AGACT AT GCTTCTCT TCTGA TA CGAAGAGA
GAM23	GIT2	3'	AGAGAAGCATCAGTCT	232	C CAA AGACT AT GCTTCTCT TCTGA TA CGAAGAGA
GAM23	GRID1	3'	AGAGAAGCCTAGGTGGCT	285	A AA_ AA_ AG CTCATC GCTTCTCT TC GGGTGG CGAAGAGA ATC
GAM23	GT650	3'	AAGCTTCTATGAGTTTG	230	C_ AAGCTT CAGACTCAT AAGCTT GTTTGAGTA TTCGAA TCT
GAM23	IKKE	3'	AGGACTGTGAGTCTG	124	CA C CAGACTCAT AG TTCT GTCTGAGTG TC AGGA
GAM23	KIAA0254	5'	AGAGGACCGGATGATC	131	AA_ GC_ TTCTCT GACTCATC GC TTCTCT CTGAGTAG CG AGAGA CC
GAM23	KIAA1026	3'	AGAGAAGCTGCCTCAGTCTG	292	CATCA CAGACT AGCTTCTCT GTCTGA TCGAAGAGA CTCCG
GAM23	KIAA1163	3'	AGAGAAGCATGTCTGAGTT	331	T_ A GACTCA CA GCTTCTCT

GAM23	KIAA1598	3'	AGAAAGCTTCTGTGTTTTGGGTCTG	161	TTGAGT GT CGAAGAGA CT A TC CAGACTCA AAGCTTCT GTC TGGGT TTCGAAGA TTTGTC CAA CAGACTCAT GCTTCT GTCTGGGT CGAAGA A CT A GA CATCA GCTTCTCT CT GTGT CGAAGAGA AG CA A CAGACT TCA GCTTCTCT GTTTGA AGT CGAAGAGA G TCA GACT CA AGCTTCTCT TTGA GT TCGAAGAGA A TTC A A CAG CTC TCAA GCTTCT GTC GAG AGTT CGAAGA C T CA CAGACTCAT AGCTTCT GTCTGAGTG TCGGAGA
GAM23	KIAA1853	3'	AGAAGCAATGGGTCTG	287	C CA GA TC AT AGCTTCTCT CT AG TG TCGAAGAGA A A AC A A AA CAG CTC TC GCTTCTCT GTC GAG AG TGAAGAGA C A GA ATCAA CAGACTC GCTTCTCT
GAM23	LOXL4	3'	AGAGAAAGCTGTTGGATC	213	
GAM23	METAP1	3'	AGAGAAAGCTGAAAGTTG	298	
GAM23	MGC11034	3'	AGAGAAAGCTCTTTTGAAGTT	211	
GAM23	MGC14128	3'	AGAAGCTTTGAGAGCCCTG	222	
GAM23	MGC16175	5'	AGAGGCTGTGAGTCTG	219	
GAM23	MGC2752	5'	AGAGAAAGCTCAGTAGAATC	327	
GAM23	MGC34923	3'	AGAGAAAGTAGGAAGAGCCTG	254	
GAM23	NR113	5'	AGAGAAAGCAGGAGTCTG	89	

GAM23	NYD-SPI5	3'	AGAGAAAGAAATATTTGAGTCTG	208	GTCTGAG CGAAGAGA GA TCAAG CTTCTCT CAGACTCA GTCTGAGT GAAGAGA TTATAAA ATCAA CAGACTC GCTTCTCT GTCTGGG TGAAGAGA GT CA CT CAGACTCAT AG TCTCT GTCTGAGT TC AGAGA CC AGCT CAGACTCA TCA TCTCT GTCTGAGT AGT AGAGA T TCAA T CAGACTCA GCT CTCT GTCTGAGT CGA GGA CT TCA CAGA CA AGCTTCTCT GTCT GT TCGAAGAGA AT TTC A AA CAG CTCATC GCTTCTCT GTC GAGTAG TGAGGAGA C G TCAA C CAGACTCA GCTT TCT GTCTGGGT CGAA AGA TTTGGG A CT T CAGA CA CAAGCTTCTCT GTTT GT GTTCGAAGAGA TT GC CAGACTCAT CAA TCTCT
GAM23	OSBPL8	5'	AGAGAAAGTTGGGGTCTG	177	
GAM23	PLEKHA4	5'	AGAGACCCCTGTGAGTCTG	178	
GAM23	PRKWNK2	3'	ACAGATGATTGAGTCTG	372	
GAM23	PSMD4	3'	AGGGTAGCTGAGTCTG	63	
GAM23	RIS1	3'	AGAGAAAGCTCTTTGTATCTG	337	
GAM23	RNF24	3'	ACAGGAGTGGATGAGCCTG	114	
GAM23	SNURF	3'	AGAAAAAGCGGTTTTTGGGTCTG	96	
GAM23	SULT4A1	3'	ACAGAAAGCTTGTGTTTTTG	284	
GAM23	SV2B	3'	ACAGAAATTGTGTGAGTCTG	135	

GAM23	SZF1	5'	AGAGAAAGCCTAGATATCTG	147	GTCTGAGTG GTT AAGAGA T CTC AA CAGA ATC GCTTCTCT GTCT TAG CGAAGAGA A ATC A TCAAG CAGACTCA CTTCTCT GTCTGAGT GGAGAGA TATG C T GA TCA CAAGCTTCTCT CT AGT GTTCGAGGAGA A AAG CAGACTCATC CTTCT GTTTGAGTAG GAAGA
GAM23	TLR10	5'	AGAGAGGGTATTGAGTCTG	210	
GAM23	ZNF185	3'	AGAGGAGCTTTGTGAATC	111	
GAM23	LOC113612	3'	AGAAAGATGAGTTTG	300	
GAM23	LOC133539	3'	AGAGAAAGCCAGGATGGTC	312	T AA GAC CATC GCTTCTCT CTG GTAG CGAAGAGA GACC AC CAA CAG TCAT GCTTCTCT GTC AGTA CGAAGAGA C CA CAGACTCAT CAA GCTT GTCTGAGTA GTT TGAA AT ATT AA T CAGACTCATC GCT CTCT GTCTGAGTGG TGA GAGA GGG A ATCA CAG CTC AGCTTCTCT GTC GAG TCGAAGAGA AACGG CA C GACT TCAAGCTT TCT
GAM23	LOC139221	5'	AGAGAAGCACATGACCCTG	313	
GAM23	LOC142941	3'	AAGTTTATTGTAATGAGTCTG	345	
GAM23	LOC145717	5'	AGAGAGTGGGGTGAGTCTG	279	
GAM23	LOC147229	3'	AGAGAAGCTGGCAAGAGCTG	325	
GAM23	LOC147658	3'	AGAAAAGTTTGAAGTC	326	

Accession	Position	Sequence	Length
GAM23	LOC147920 3'	AGAGAAAGCCTGAGGAATTT	328
		CTGA AGTTTGAA AGA C A A AGA TC TCA GCTTCTCT TTT AG AGT CGAAGAGA A G C A CA CAG CTCAT AGCTTCTCT GTC GGGTG TCGAAGAGA C CC C A CAGA TCATC AGCTTCTCT GTCT AGTGG TCGAAGAGA G	
GAM23	LOC148894 5'	AGAGAAAGCTCCGTGGGCCTG	347
		T T GAC CA CAAGCTTCTCT CTG GT GTTCGAAGAGA	
GAM23	LOC150606 3'	AGAGAAAGCTGGGTGATCTG	349
		C - CTCTCTCT AGA TCATCAAG CTCT TTT AGTAGTTC GAGA A TTTAT A ATCA CAG CTC AGCTTCTCT GTC GAG TCGAAGAGA GACG - CAA T AGACTCAT GCT CTCT TCTGAGTA CGG GAGA AAG AA - T CAGACTCAT GCT CTCT GTCTGAGTGG TGA GAGA GGG A A AA CAG CTC TC GCTTCTCT GTC GGG AG CGAAGAGA G G CC GACTCATC GCTT TCT 	
GAM23	LOC150606 3'	AGAGAAAGCTTGTGGTC	350
GAM23	LOC152220 3'	AGAGTATTTCTTGATGAATTT	351
GAM23	LOC155382 3'	AGAGAAAGCTGCAGGAGCTG	356
GAM23	LOC157621 3'	AGAGGGCGAAATGAGTCT	358
GAM23	LOC161528 5'	AGAGAGTGGGGTGAGTCTG	342
GAM23	LOC197114 5'	AGAGAAAGCCCGAGGGGGCTG	369
GAM23	LOC199883 3'	AGAAAGGCGGTGAGTC	370

GAM23	LOC200020 3'	AGAAAGCGGTGAGTC	371	CTGAGTGG CGGA AGA A AA C GACTCATC GCTT TCT CTGAGTGG CGGA AGA
GAM23	LOC200226 3'	AGAGAACTCGTGAATGTT	365	A CA GAC TCAT AGCTTCTCT TTG AGTG TCGAAGAGA
GAM23	LOC204820 5'	AGAGAAAGCCAGGCCAGCTG	373	TA C A CA AA CAG CT TC GCTTCTCT GTC GA GG CGAAGAGA
GAM23	LOC219392 5'	AGAGAAATCCTAGATGAGTC	377	- CC AC A C GACTCATC AG TTCTCT CTGAGTAG TC AAGAGA
GAM23	LOC219800 3'	AGAGAACTTTGGGAGCCT	389	A A CTA A A AG CTC TCAAGCTTCTCT TC GAG GGTTCGAAGAGA
GAM23	LOC220753 5'	AGAGAAAGCCAGAGGTGTG	388	C G CA AA CA ACT TC GCTTCTCT GT TGG AG CGAAGAGA
GAM23	LOC220776 3'	AGAGGGGTGATGATAAACTG	283	G AC AC AA CAG TCATC GCTTCTCT GTC AGTAG TGGGGAGA
GAM23	LOC221454 5'	AGAGAAAGATGAAGTTTG	382	AAAT CA AG CAGACT TCA CTTCTCT GTTTGA AGT GAAGAGA
GAM23	LOC222444 3'	AGAGAAAGCCAGGATGCTC	392	A A T AA GAC CATC GCTTCTCT CTG GTAG CGAAGAGA
GAM23	LOC222962 3'	AGAGGGGAGGTAAGTCTG	387	- C AAG GACC CAGACT ATC CTTCTCT

Gene	Chromosome	Position (kb)	Sequence (5' to 3')	Distance (bp)	Sequence (3' to 5')	Distance (bp)
GAM23	LOC245727	5'	AGAGAGTGGGGTGAGTCTG	376	GTCTGA TGG GGGGAGA A A__ T CAGACTCATC__GCT CTCT GTCTGAGTGG TGA GAGA GGG CATCA CAGACT AGCTTCTCT GTTTGG TCGAAGAGA ACG__ CTCAT CAGA CAAGCTTCTCT GTTT GTTTGAAGAGA AAAT__ATCAA CAGA__CTC GCTTCTCT GTCT GAG CGAAGAGA C C__C A A__C AG CTCATCAAG__TTCT TC GAGTAGTTC AAGA A CC CAGACTCATC CTTCT GTTTGAGTAG GAAGA A__C__A III TG GA__AC__CAG TTGTA T AC CT TG GTC AACAT A TATAC TA C III C__C__A III TG GA__AC__CAG TTGTA T AC CT TG GTC AACAT A TATAC TA C III A A C TCC AA TG GAACCCAG AGG TT AC CTTGGGTT C C__ G C__ TGC AA__CCAGATTGTA 	
GAM23	LOC253525	5'	AGAGAAAGCTGCAGGTTTG	401		
GAM23	LOC254249	5'	AGAGAAAGTTTGTAAATTGG	397		
GAM23	LOC255475	5'	AGAGAAAGCCGAGCTCTG	403		
GAM23	LOC51026	3'	AGAAACCTTGATGAGACT	146		
GAM23	LOC91308	5'	AGAAGAGATGAGTTTG	274		
GAM24	CASP10	3'	ATACAACTGATGTCATATTCC ATTTTGGA	223		
GAM24	CASP10	3'	ATACAACTGATGTCATATTCC ATTTTGGA	224		
GAM24	CHRN3	5'	TTGGGTTCCACTTCGGA	49		
GAM24	LANCL1	3'	TACAACTGGGACTTTGGTA	100		

GAM24	MS4A3	3'	ACATCTGGGTTCAAATTCTG	101	ATG TT GGTCTAACAT G CA A GC T CA AAT GAACCCAGAT GT GT TTA CTGGGTCTA CA C AA CCA ATGCGAAC GATTGTA TACGCTTG TTAACAT ACCTG A C AGA TCCA AATGCGAA CC TTGTA GGGT TTACGCTT GG AACAT C TA
GAM24	SLC1A4	3'	TACAAATTGTCCAGTTCGCAT	64	TCCA AATGCGAA CC TTGTA GGGT TTACGCTT GG AACAT C TA
GAM24	ALLC	5'	TACAAGGATTTCGCATTCTGGG	162	TCCA AATGCGAA CC TTGTA GGGT TTACGCTT GG AACAT C TA
GAM24	APOL6	3'	CTGGGTTTACATTCTTGA	206	TCCA AATGCGAA CC TTGTA GGGT TTACGCTT GG AACAT C TA
GAM24	CBX6	3'	TTGGGCTCCATTCTGGA	128	TCCA AATGCGAA CC TTGTA GGGT TTACGCTT GG AACAT C TA
GAM24	FLJ10055	3'	TTGGGAGTCCCATTTTGA	156	TCCA AATGCGAA CC TTGTA GGGT TTACGCTT GG AACAT C TA
GAM24	FLJ22059	5'	CAGTCTGGACCGACCTTGA	191	TCCA AATGCGAA CC TTGTA GGGT TTACGCTT GG AACAT C TA
GAM24	KCNH8	3'	TTGGGTTTCCATTCTGGA	252	TCCA AATGCGAA CC TTGTA GGGT TTACGCTT GG AACAT C TA
GAM24	KIAA0870	3'	TTGGGTTTCCATTCTTGA	339	TCCA AATGCGAA CC TTGTA GGGT TTACGCTT GG AACAT C TA
GAM24	KIAA1157	3'	ACAGTATTCCATTCTTGA	296	TCCA AATGCGAA CC TTGTA GGGT TTACGCTT GG AACAT C TA

GAM24	PRO1048	3'	ACAATGAGTTTGCATTTT	163	AGGTTTTTAC CTT TGACA - C GA AAAAATGCGAAC CA TTGT TTTTACGTTTG GT AACA
GAM24	PRO1787	3'	ACAAATCCGCATTTTG	165	A AACCCA CAAAATGCG GATTGT GTTTTACGC TTAACA
GAM24	UBE2G1	3'	TACAGATGATTACGCATTTTG	67	C AACC GA CAAAATGCG CA TTGTA GTTTTACGC GT GACAT
GAM24	LOC122402	3'	TACTTCTTGGTTTCACATTTTGG	306	ATTA A C C TT TCCAAAATG GAACC AGA GTA AGGTTTTTAC CTTGG TCT CAT
GAM24	LOC153592	3'	GGAAATTCAGCATTTTGGGA	355	A T T C C TCCAAAATGC GAA CC AGGTTTTTACG CTT GG
GAM24	LOC256158	5'	ACAAATCTGAACGTCCTGGG	404	A AA AAAT AACCC TCCA GCG CAGATTGT GGGT TGC GTCTAACA
GAM25	ITGA5	3'	CTCAGATCCAGGGACAGAGG	264	C AA GTTAGA A TCTCTG CC GATCTGAG GGAGAC GG CTAGACTC
GAM25	SF3B3	3'	GCTCTAGAATCTTAACCAGA	116	AG AC CCAGA TCTGGTTTGA TCT GAGC AGACCAATCT AGA CTGG
GAM25	SLC4A4	3'	GCTCAGAGTTGTTTAACCAGA	71	A T AC A TCTGGTTTGA CAG TCTGAGC AGACCAATT GTT AGACTCG
GAM25	ZNF180	3'	CTCAGACCTGAATCAGAGA	120	AGAC A TCTCTGGTT CAG TCTGAG

GAM25	AP1G2	5'	GCCCAGGCACGCCCGACCAGAG	233	AGAGACTAA	GTC	AGACTC
			A		AGACCAGA	A	
					TCTCTGGTT	TCTG	GC
					AGAGACCAG	GGAC	CG
					CCCGCAC	C	
GAM25	BCL2L1	3'	GCCCAGATCTGGTCCCTTGACAG	241	GTTA	A	
					CTG	GACCAGATCTG	GC
					GAC	CTGGTCTAGAC	CG
					GTTC	C	
GAM25	FLJ25012	5'	CTCAGATCTGAAAAAGCACAAGA	250	TCT	AGAC	
					TG	CCAGATCTGAG	
					AGA	GTCTAGACTC	
					AC		
GAM25	FLJ31952	3'	CAAATCTGGTTCTGAAAG	253	GG	C	
					CT	CCAGAT	TG
					GA	GGTCTA	AC
					A	A	
GAM25	MDS025	3'	CTCAGACCTGGTTTGAGATAGA	184	TCTG	TCTGAG	
					AGAT	AGTTGGTC	AGACTC
					AG	C	
GAM25	MGC32043	3'	GCTCAGATCTGATGCTTCAAGA	249	GGTT	AC	CAGATCTGAGC
					AGA	TC	GTCTAGACTCG
					ACT	GTA	
GAM25	MSI2	3'	CTCCCCATCCCAACCAGAGA	245	TCTCTGGTT	GAT	GAG
					AGAGACCAA	CTA	CTC
					CC	CCC	
GAM25	ZNF271	5'	GCTCAGATCTGGTTAAACATCA	395	TCTCTG	GTT	GACCAGATCTGAGC
			GAGA				
					AGAGAC	CAA	TTGGTCTAGACTCG
					TA	A	
GAM25	LOC144508	5'	GCTCAGATCCATGTGCCAGGGA	362	TCTCTGGT	GATCTGAGC	
					AGGGACCG	CTAGACTCG	
					TGTAC		
GAM25	LOC145845	3'	CTCAAAATCCCAACCAGAGA	346	TCTCTGGT	GAT	TGAG

GAM26	CDH19	3'	GAAAAATTTAAAGGAGCAA	182	AGAGACCA CTA ACTC CC A A CTTTAAATTTTC TTTTCCCA AACG GAAATTTTAAAG AG T CTTTAA TTTTCCCA TTGGT GCA AAAAGGGT AACCA CGT ATCTGACC - C A TTGGTTG ACTTT AATTTTC TTTTCC AATCAAC TGAAA TTAAAG A AG TTGGTTGCA TTT TTTTCC AAAAGG AACCAACGT AGA C AA CTTTAA TTGGTTGCA ATTTTC TAGAAG AACCAACGT AA GC TAAATTT TCCCA TTGGTT ACTT AGGGT AACCA TGAA A C TT GCACTTTAAATTTTC CA GTGAAATTTAAAG GT GATC TT A GC TTAA TTTTCCC TTGGTT ACT AAAAGG AACCA TGA A CG ATT G CACTTTAA TTCC GAGG AACCA GTGAAAT G AT TTGGTTGC CTTT TTTTC
GAM26	CRYGS	5'	TGGGAAAACCACTCTATGCACC	152	AA
GAM26	CYP1B1	3'	GAAAAATTGAAAAGTACAACCTAA	33	
GAM26	GLI3	3'	GGAAAAAAGACTGCAACCAA	35	
GAM26	PCLO	3'	GAAGATAATGCAACCAA	391	
GAM26	PPP2R5A	3'	TGGGAAAGTAAACCAA	102	
GAM26	PTER	3'	TGAGAAAATTTAAAGTGTTTCT	207	AG
GAM26	RFX5	3'	GGGAAAAGCAGTAAACCAA	39	
GAM26	CSMD1	3'	GGAGTATTAAAGTGGAACCAA	301	
GAM26	MGC15438	3'	GAAAGAAAGCGCAGCCAA	220	

GAM26	NYD-SP18	3'	GGAGAAAACTGCAACCAA	217	AACCGACG GAAA GAAAG C C AAAT TTGGTTGCA TTT TTTCC AACCAACGT AAA AGAG C C TAAA TTGGTTGCA TT TTTTCC AACCAATGT AA AAAAGG TA CACTTTAA TTGGTTG ATTTTCCC AACCAAC TAGAAGGG ACG A TAA TTGGTTGC CTT ATTTT AACCAACG GAA TAAGA C CAGG G G ATTT TTGGTT CACTTTAA TCC AACCA GTGAAATT AGG G AC AAT TTGGTTGC TTTA TTTCC AACCAACG AAAT AAAGG GT ATT TAA TTGGTTGCACCTT ATTTT AACCAACGTGAA TAAAG CGG C CCC C GG AACGA CT GTCACAAT CC TTGTT GA CAGTGTTA A AA A TGGCAAC GACCC CT GT ACCGTTG CTGGG GA CG T G CTGTC TGGCAAC ACCC ACAATA
GAM26	OLF3	3'	GGAAAAAATAATGTAACCAA	340	
GAM26	RPL13A	3'	GGGAAGATGCACAACCAA	115	
GAM26	LOC129452	3'	AGAAATGGACAAGCGCAACCAA	310	
GAM26	LOC150197	3'	GGATTAAAGTGAACCAA	335	
GAM26	LOC162239	3'	GGAAATTATAAATGGCAACCAA	344	
GAM26	LOC219972	3'	GAAATGGCAAGTGCAACCAA	379	
GAM27	DDX6	3'	ATTGTGACAAGAATTGTTACC	80	
GAM27	LOC126917	3'	GCAGTGGTCTGTTGCCA	309	
GAM27	LOC170395	3'	TATTGTTTCTGGGTGTTGCCA	316	

GAM28	ABCC3	3'	TGCCCCCTGGCTGTGCTCTAC	170	<p>ACCGTTG TGGG TGTAT</p> <p>C A_ T TCIT_</p> <p>GTG AG ACA CCAGGGGCA</p> <p> </p> <p>CAT TC TGT GGTCCCGT</p> <p>C G C</p> <p>AGAAC_ ATCCAGGGGCA</p> <p> </p> <p>TACG TAGGTCCCGT</p> <p>ACCATC</p> <p>AGAAC_ ATCCAGGGGCA</p> <p> </p> <p>TACG TAGGTCCCGT</p> <p>ACCATC</p> <p>CA AC</p> <p>TAGTG GA ATCCAGGG</p> <p> </p> <p>ATCAC CT TAGGTCCC</p> <p>A_ CC</p> <p>CA AC</p> <p>TAGTG GA ATCCAGGG</p> <p> </p> <p>ATCAC CT TAGGTCCC</p> <p>A_ CC</p> <p>CA AC</p> <p>TAGTG GA ATCCAGGG</p> <p> </p> <p>ATCAC CT TAGGTCCC</p> <p>A_ CC</p> <p>CA AC</p> <p>GTG GAACA_ TCCAGGGGCA</p> <p> </p> <p>CAT TTTGT AGGTCCCGT</p> <p>CC AC</p> <p>G CA</p> <p>TAGT CAG AACATC GGGGCA</p> <p> </p> <p>GTC GTC TTGTAG CCCCCT</p> <p>G C AC</p> <p>T C CA</p> <p>A AGTG AGAACATC GG</p> <p> </p> <p>A TCAC TCTGTGG CC</p> <p>C A A_</p> <p>TATAGTCAGA AT CCA</p> <p> </p> <p>ATATCACGTCT TA GGT</p> <p>CAT C</p> <p>CA</p> <p>AGTGCAGAA TCCA_ GGGGCA</p> <p> </p>
GAM28	CASP3	3'	TGCCCCCTGGATCTACCAGCAT	225	
GAM28	CASP3	3'	TGCCCCCTGGATCTACCAGCAT	79	
GAM28	EMS1	3'	CCCTGGATCCTCACACTA	90	
GAM28	EMS1	3'	CCCTGGATCCTCACACTA	240	
GAM28	MLLT2	3'	TGCCCCCTGGACATGTTTCCTAC	97	
GAM28	TACC1	3'	TGCCCCCAGATGTTCTGGGCT	104	
GAM28	TNFSF6	3'	CCAGGTGTTCTACACTCA	42	
GAM28	UBB	3'	TGGCATTACTCTGCCTATA	166	
GAM28	AKAP10	3'	TGCCCCCTTTGGAATTCTGCACT	113	

GAM28	DECR2	3'	GCCCCCTCTGTCTCTGCACT	176	TCACGTCCTT AGGT CCCCCT A TT A TCC GTGCAGA ACA AGGGC CAGTCT TGT TCCCCG
GAM28	KIAA0240	3'	GCCCCCTGTGTCCCACTA	383	C C CA A TC TAGTG GA CA CAGGGC ATCAC CT GT GTCCCCG
GAM28	MGC16385	5'	GCCCCCTGGACGTTTCTGTCCGC	255	C _ _ A GTG CAGAA C TCCAGGGC CGC GTCCT G AGTCCCCG
GAM28	MGC5139	5'	GCCCCCTGGGCACACTGTA	305	C T C CAGAAC TATAGTG TCCAGGGC ATGTCAC GGTCCCCG
GAM28	P5-1	3'	CCCCCTGGATGCCCTTAACCACT	110	AC _ _ C AA AGTG AG CATCCAGGG TCAC TC GTAGTCCCC
GAM28	TED	3'	CCCCCTGGGCCCTGCCCTA	143	CAA CCC T AACA TAG GCAG TCCAGGG ATC CGTC GGTCCCC
GAM28	LOC133418	3'	TGCTCTAAAGCTCTGCACTA	311	CC _ _ ACATCCA TAGTGCAGA GGGCA ATCACGTCT TCTCGT
GAM28	LOC152402	3'	GCCCCCTTACATTCTGCACT	353	CGAA _ CATCC AGTGCAGAA AGGGC TCACGTCTT TTCCCCG
GAM28	LOC158677	3'	TGCCCCCTGGATATCAGCAATAT	360	ACA _ G A AC TATA TGC GA ATCCAGGGCA ATAT ACG CT TAGTCCCCGT
GAM28	LOC221715	3'	CCACTGTGCTTGCACTA	390	A A A AA TC TAGTGCAG CA CAG GG

GAM28	LOC254746	3'	TGGCATTACTCTGCACTATA	394	ATCAGGTT GT GTC CC C AC A TATAGTCAGA AT CCA ATATCACGTCT TA GGT CAT C ACATCCA TAGTGCAGA GGGGCA ATCACGTCT TCTCGT CGAAA AG TATGG GCCTT GCATCTCC CAG CGGAA CGTAGAGG GTC CT TA AGCCTTAGGC CT TGGCA TCGGAATCCG GA ACCGT C
GAM28	LOC255098	3'	TGCTCTAAAGCTCTGCACTA	396	AGC TTAGGCATC TCC TCG AATCCGTAG AGG A TGA GCCTTAGG TCCTC TGG CGGAGTCC AGAG ACC AC CTA GCCTTAGG TCCTC TGG CGGAGTCC AGAG ACC AC GCCTTAGG TC CCT GGCAG CGGAATCC AG GGA CCGTC AC CCC CA T AT TTA CT G AGCC GGCATCTC AT GC TCGG CCGTAGAG TG TG CAC T G T CTCCT AGCCT AGGCAT ATGGCAG
GAM29	ADAM19	3'	CTGATGGAGATGCTCAAGGC	228	
GAM29	LFG	3'	TGCCACAGGCCCTAAGGCT	319	
GAM29	NOLA2	5'	GGAAGTGATGCCCTAAAGCT	393	
GAM29	FLJ10751	3'	CCAGAGACACCTGAGGC	158	
GAM29	FLJ10751	3'	CCAGAGACACCTGAGGC	159	
GAM29	FLJ10925	5'	CTGCCCCCAGGGACACCTAAGG	160	
GAM29	KIAA1118	3'	GTGGTTGAGATGCCACGGCT	289	
GAM29	KIAA1649	3'	CTGCCATTTCTGTGCCTAGGCT	215	

GAM29	LIMR	3'	CTGCCATCTGCTGCTAGGC	157	TCGGG TCCGTG TACCGTC T ⁻ TCTCCT ⁻ TCCTT ⁻ GCCT AGGCA ATGGCAG CGGA TCCGT TACCGTC CGTC
GAM29	MGC14161	5'	CCAGAGAGATGCCAAAGGC	221	A ⁻ CTA ⁻ GCCTT GGCATCTC TGG CGGA CCGTAGAG ACC
GAM29	NJMU-R1	3'	CATGAAGAAATGCCCTGAAGC	188	A ⁻ AG ⁻ C C C ⁻ C ⁻ GC TTAGGCAT TC TATG CG AGTCCGTA AG GTAC
GAM29	SEMA3E	3'	CTGTTGTGAGAAATGCCCAAGC	119	A TA C C TG AGCCT GGCAT TC TA GCAG TCGGA CCGTA AG GT TGTC C ⁻ A A GT ⁻ CATCTC
GAM29	YKT6	3'	CTGCCATAGATACCCTAAG	106	CTTAGG CTATGGCAG GAATCC GATACCGTC CATA ⁻
GAM29	LOC142972	5'	GCCACAGGAGATGCCCAAGC	271	C A A GC TT GGCATCTCCT TGGC CG AA CCGTAGAGGA ACCG A C C AG ATCTCC AGCCTT GC TATGGCA TCGGAA CG ATACCGT CT A ⁻ A ⁻ T ⁻
GAM29	LOC143689	3'	TGCCATAAGCTCAAGGCT	318	CTTAGGC TC CCTATGG GAATCCG AG GGATACC
GAM29	LOC148930	5'	CCATAGGAGCCTAAG	332	
GAM29	LOC220469	3'	CCAAGGATGCCCAAGC	317	C A ⁻ T ⁻ A ⁻ GC TT GGCATC CCT TGG CG AA CCGTAG GGA ACC A C CAT ⁻ C ⁻
GAM29	LOC253782	3'	CATAAGACCACTAAGC	398	GCCTTAGG CTC TATG

CGGAATCC GAG ATAC
AC A
A CCTAT
AGCCTTAGGC TCT GGCA
|||||
TCGGAATCCG AGA CCGT
G C

GAM29 LOC92078 5' TGCCCAGAGGCCCTAAGGCT 282